

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/686,490D

Source: TFMO

Date Processed by STIC: 3-25-05

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 03/25/2005

PATENT APPLICATION: US/10/686,490D

TIME: 08:16:07

Input Set : A:\35991.ST25-US.rtf - sequence listing.txt

Output Set: N:\CRF4\03252005\J686490D.raw

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3 <110> APPLICANT: Bayer Aktiengesellschaft
W--> 4 <120> TITLE OF INVENTION: Anti-Kazlauskas-Lipases
W--> 5 <130> FILE REFERENCE: LeA 35 991
C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/686,490D
C--> 6 <141> CURRENT FILING DATE: 2003-10-15
W--> 6 <160> NUMBER OF SEQ ID: 2
7 <170> SOFTWARE: PatentIn version 3.1
9 <210> SEQ ID NO: 1
10 <211> LENGTH: 885
11 <212> TYPE: DNA
12 <213> ORGANISM: unknown
W--> 13 <220> FEATURE:
14 <221> NAME/KEY: CDS
15 <222> LOCATION: (1)..(885)
16 <223> OTHER INFORMATION: bacterial
18 <400> SEQUENCE: 1
19 atg gca cag gtg aag gcc aac ggc att acc ctc gag tat gaa gag cag      48
20 Met Ala Gln Val Lys Ala Asn Gly Ile Thr Leu Glu Tyr Glu Glu Gln
21 1      5      10      15
23 ggc cat cgc cac cat ccg tcc atg ctc ctc att atg ggc ctg ggc ggc      96
24 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
25      20      25      30
27 cag tta atc gac tgg ccc gag gag ttc atc cgg ggg ctg gct gaa cga      144
28 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
29      35      40      45
31 ggc ttc cgg gta atc tgt ttc gac aac cgc gac gcg ggg ctt tcg acg      192
32 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
33      50      55      60
35 aaa ctt gaa ggc gtg aaa aaa ccg aac att gcc cgg gta ttt ctc ctg      240
36 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
37 65      70      75      80
39 gcg agc atg ggc cta aag ccc agg gtg cct tac acc ctc gac gac atg      288
40 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
41      85      90      95
43 gcc ctg gac acc gtg ggg ctg atg gat gcc ctg ggc att gag agc acc      336
44 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
45      100      105      110
47 cac gta gtt ggc gtc tcc atg ggc ggc atg att gcg cag att cta ggg      384
48 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
49      115      120      125
51 gcg aag cac ggg gag cgg gtg aaa tcc ctt acc ctg atg att acc tcc      432
52 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
53      130      135      140

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55 tcc ggc aac ccc cgc atg ccg gcg ccc agg ccg cag gtg ctg caa aag      480
56 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
57 145                      150                      155                      160
59 ttt atg cgg gtg ccc aag agc atg gat aag gaa gag tgg att aaa tac      528
60 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
61                      165                      170                      175
63 aac ttg gag ctt tta acc acc atc ggc agc ccc ggg ttg gac cgg gag      576
64 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
65                      180                      185                      190
67 aag ctg gcc tta gac gtg agg aag agc ata gag cgg tgc ctt tgc ccc      624
68 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
69                      195                      200                      205
71 gaa ggc acg cag cgg cag ctg gca gcc atc ctg cag agc ggc agc agg      672
72 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
73                      210                      215                      220
75 gtg aag ctg ctc cgg cgg atc gct gtc ccc acc ctg gtc atc agc ggg      720
76 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
77 225                      230                      235                      240
79 gcg gaa gat ccc ctc ctg ccg tac cag tgc ggc cgg gac att gcc gac      768
80 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
81                      245                      250                      255
83 cat atc ccg gga gcc cgc ttc gag ctc atc gag ggc atg ggg cac gac      816
84 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
85                      260                      265                      270
87 att ccc gag cgg cac atc ccc cgg ctg att gag ctc atc gcc ggg cac      864
88 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
89                      275                      280                      285
91 gcc gcg gcc gcg gaa gct taa      885
92 Ala Ala Ala Ala Glu Ala
93                      290
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 294
98 <212> TYPE: PRT
99 <213> ORGANISM: unknown
101 <220> FEATURE:
102 <223> OTHER INFORMATION: bacterial
104 <400> SEQUENCE: 2
106 Met Ala Gln Val Lys Ala Asn Gly Ile Thr Leu Glu Tyr Glu Glu Gln
107 1                      5                      10                      15
110 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
111                      20                      25                      30
114 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
115                      35                      40                      45
118 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
119                      50                      55                      60
122 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
123 65                      70                      75                      80
126 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
127                      85                      90                      95

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130 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
131          100          105          110
134 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
135          115          120          125
138 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
139          130          135          140
142 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
143 145          150          155          160
146 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
147          165          170          175
150 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
151          180          185          190
154 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
155          195          200          205
158 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
159          210          215          220
162 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
163 225          230          235          240
166 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
167          245          250          255
170 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
171          260          265          270
174 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
175          275          280          285
178 Ala Ala Ala Ala Glu Ala
179          290

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VERIFICATION SUMMARY

DATE: 03/25/2005

PATENT APPLICATION: US/10/686,490D

TIME: 08:16:08

Input Set : A:\35991.ST25-US.rtf - sequence listing.txt

Output Set: N:\CRF4\03252005\J686490D.raw

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L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:6 M:283 W: Missing Blank Line separator, <160> field identifier
L:13 M:283 W: Missing Blank Line separator, <220> field identifier